

OM of: US-09-494-297-2 to: Issued\_Patents\_NA:\* out\_format : pfs  
Date: Jun 6, 2001 11:27 PM

About: Results were produced by the GenCore software, version 4.5,  
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## Command line parameters:

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## Search information block:

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Query length: 757  
Database: Issued\_Patents\_NA:\*  
Database sequences: 302621  
Search time (sec): 76.790000

## score\_list:

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## seq\_documentation\_block:

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; Sequence 2, Application US/08867941  
; Patent No. 5977337  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M  
; APPLICANT: Du, Run-Pan  
; APPLICANT: Wang, Qun-Jun  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/867,941  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; TELECOMMUNICATION INFORMATION: 1038-681 MIS:jb  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2694 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-867-941-2
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## alignment\_scores:

Quality	178.00	Length: 918
Ratio:	0.467	Gaps: 42
Percent Similarity:	41.503	Percent Identity: 18.627

alignment\_block:  
US-09-494-297-2 x US-08-867-941-2

Align seg 1/1 to: US-08-867-941-2 from: 1 to: 2694

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313 .....GCTAA 318
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; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M

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; APPLICANT: Run-Pan Du
; APPLICANT: Quijun Wang
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2694 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; US-09-074-658-2

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Quality: 178.00      Length: 918
Ratio: 0.467        Gaps: 42
Percent Similarity: 41.503      Percent Identity: 18.627

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1274 CTAAAT..... 1278
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332 .....IleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeu 345
1361 ATGTGCTCTTGTGGTGAACGAGACAAAACAGCAACACCTGTGCACA 1410
346 ThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrP 362
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seq_documentation_block:
  Sequence 1, Application US/09074658
  Patent No. 6184371
  GENERAL INFORMATION:
    APPLICANT: LOOSMORE, Sheena M
    APPLICANT: Run-Pan Du
    APPLICANT: QulJun Wang
    APPLICANT: yang, Yan-Ping
    APPLICANT: Kleih, Michael H
    TITLE OF INVENTION: LACTOERRIN RECEPTOR GENES OF MORAXELLA
    NUMBER OF SEQUENCES: 78
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Slim & McBurney
      STREET: 6th Floor, 330 University Avenue
      CITY: Toronto
      STATE: Ontario
      COUNTRY: Canada
      ZIP: M5G 1R7
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/074, 658
      FILING DATE: 08-MAY-1998
      CLASSIFICATION: 435
    ATTORNEY/AGENT INFORMATION:
      NAME: Stewart, Michael I
      REGISTRATION NUMBER: 24,973
      REFERENCE/DOCKET NUMBER: 10308-795

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7650 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-074-6558-1

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      Ratio: 0.467      Gaps: 42
Percent Similarity: 41.503      Percent Identity: 18.627

alignment_block:
US-09-494-297-2 x US-09-074-6558-1 ..

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Sequence 69, Application US/09074658

Patent No. 6184371

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M

APPLICANT: Run-Pan Du

APPLICANT: Quijun Wang

APPLICANT: Yang, Yan-Ping

APPLICANT: Klein, Michel H

TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA

NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

STREET: 6th Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/074,658

FILING DATE: 08-MAY-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-795

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 2718 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-074-658-69

alignment\_scores:

Quality: 176.00 Length: 796  
Ratio: 0.515 Gaps: 40  
Percent Similarity: 42.965 Percent Identity: 20.603

alignment\_block:

US-09-494-297-2 x US-09-074-658-69 ..

Align seg 1/1 to: US-09-074-658-69 from: 1 to: 2718

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      ||| :|||
      :||| :|||
2089 . .TATATATTGACCAAAAGACTTTATCCCAAGATGACGATGATGAC 2136
520 AspSerAlaGluLeuAspIysAspIysLeuLysasp..TyrHisGlyPh 535
      ||||| :||| :||| :|||
      ||||| :||| :||| :|||
2137 GATAGTTTGGACCGCATCTGATGATTCACAAAGATGATATACATCATTGGGA 2186
535 eGlyAspMetLysAspSerThrLeuAlaValAlaLysIleLeuValGluT 552
      ||||| :|||
      :||| :|||
2187 TGAATGATTTG.....ATTGCATCTGATG 2209
552 yrlAglInaSpSerAsnProGlnLeuThrAspLeuAspPheIle 568
      :||| :||| :|||
      :||| :||| :|||
2210 ATTCAACAAGATGATGACACAGATGGCATGACGATCAGATGATGATTTG... 2256
569 ProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGln 585
      :||| :||| :|||
      :||| :||| :|||
2257 . .GGTGATGGTCCAGATGATGAGCCGCGCAGCAAGCTGATTCATGCAAG 2303
585 uAspLeuValAspIleIleThrGmetGluAspIysGluValIleProV 602
      ||||| ||| :||| :||| :|||
      :||| :||| :||| :|||
2304 TAAAT.....ATTGCCCTGGAATTTGAAACAAATACTTGCACA 2341
602 aI.....ThrHisAsnLeuThrLeu..... 608
      :||| :||| :|||
      :||| :||| :|||
2342 TTATATGAGCTTACTCATGAAAAAAACCTTTGGCCCTAGATGCTAAAAAATAG 2391
609 .....ArgLysThrValThrGlyLeuAlaGln 617
2392 GCCTAAGTTTGATTAACCTTTGACACACACAGCCTTAAGTGTAAATTAA 2441
617 yAspArgThrLysAspPheHisPheGlnIleGluLeuLysAsnAsnLysG 634
      :||| :||| :||| :||| :|||
      :||| :||| :||| :||| :|||
2442 CGATGAGAGAGGCGATGATCGCTTTGATATC.....AAAATGGCAAAA 2485
634 InuIleuLeuSerGlnThrValLysThrAspLysTrpAsnLeuGluPhe 650
      :||| :||| :||| :||| :|||
      :||| :||| :||| :||| :|||
2486 TTATATGCGACAGATTTTACCGCCAAACCCGATGTGCCAAACTATCTGCAA 2535
651 LysAspGlyLysAlaThrIleAsnLeuLysHisGlyLysSerLeuThrLe 667
      :||| :||| :|||
      :||| :||| :|||
2536 GAAGTGGGT.....AACACCAAGGTGC..... 2559
667 uGlnGlyLeuProGlnGlyTyrSerTyrLeuValGluThrAspSerG 684
      :||| :||| :||| :||| :|||
      :||| :||| :||| :||| :|||
2560 .....GGTTTCTTATACCAACATCAAAAGATTTGATGTTTA 2593
684 InuGlyTyrLysValLysValAsnSerGlnGluValAla 696
      :||| :||| :||| :||| :|||
      :||| :||| :||| :||| :|||
2594 AGGGGCAATTTTTTTGGACCAAAAGGCGAAGAGTGGCA 2631
seq_name:/cgnl_7/Plodata/1/lna/5B_COMB.seq:US-08-714-402-1

seq_documentation_block:
/ Sequence 1, Application US/08714402
/ Patent No. 5910441
/ GENERAL INFORMATION:
/ APPLICANT: ROCHA, Claudia
/ APPLICANT: FISCHETTI, Vincent A.
/ TITLE OF INVENTION: FIBRINOCYTIN AND FIBRINOGEN BINDING
/ TITLE OF INVENTION: PROTEIN FROM GROUP A STREPTOCOCCI
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
/ STREET: P. O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404

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; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,402
; FILING DATE: 16-sep-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 016921-097
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-714-402-1

alignment_scores:
  Quality: 150.00      Length: 962
  Ratio: 0.367         Gaps: 51
  Percent Similarity: 42.516   Percent Identity: 19.854

alignment_block:
  US-09-494-297-2 x US-08-714-402-1 ..

Align seq 1/1 to: US-08-714-402-1 from: 1 to: 3531

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529  AAAACCGACCGGACTGTGACAGTACTGTTATGACGAGACGCTATACCAA 578
    35  uMetIle.....PheAlaLeuValThrSerMetValGlyAlaL 48
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
579  GTTGCTGAAATCCCTATATATGCGGAATCATCATGTAAGCAGGTCGCA 628
    48  yStrValPheGlyLeuValGluSerSerThrProAsnAlaIleAsnPro 64
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
629  AAGATGTT.....AGTAGTCTTTACAGTTGGAATAATCCC 663
    65  AspSerSerGluTyrArgTyrP.....TyrGlyTyr 75
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
664  AAAATGTCAGTGTCTTAATATGGAACAAACAGAGTTAGTAGGCGCC 713
    75  rGluSerTyrValArgGlyHisProTyrTyr.....85
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
714  AGCGGATTTTACCGCAACCATGCGGCTATTTTAAATGCTTTTGAGT 763
    86  ..LysGln.....PheArg 89
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
764  TGAACCAAAAGATAAATGCAAAACAATCAACCCAGGTGATACCTTG 813
    90  ValAlaHisPheLeuArgValAsnLeuGluGlySerArgSerTyrGlnVa 106
    :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
814  TTACAGCTGATAGCATGCTCAATCTCAAAAGT.....846
    106  LTyrcysPheAsnLeuLysLysAlaPhePro.....L 117
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
847  .....ATCAGTCAGATATCCCTAAATATCATTTACGACAGCTG 883
    117  euGlySerAspSerSerValLysLysTyrTyrLysLysHisAspGlyIle 133
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
884  CAATATGCTCGCTTGCGATGGAATAATACATGCTGAGAACATCACT 933
    134  SerThrLysPheGluAspTyrAla.....141

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934  ATCTATACCTTTCACAGATATATATTCGGGTTTAGATAAAGTCAGTTGTC 983
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141  .....141
984  TGCAGAAATTGAGCTTATTCCTAGAGAAATAAGGAAGTTGGAAATACTA 1033
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
142  .....MetSerProArgIleThrGlyAspGluLeuAsnGlnLys 154
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1034  GTATCTCAAAATTTTAAGATGACATAGTGGGAGAGATCACCCTATATAA 1083
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
155  .....LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnG 169
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1084  GGAACGGTAAATGTTCTTTATGAAATGAGAGACTAAGAAACATATA 1133
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
169  yIleMetGluGlyLeu.....GluProLeuAsnA 179
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1134  TATTACTAATGATGATGAGCAATGTGGTGAGATTTGAAGTAACCTACA 1183
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
179  IaIleArgValThrGlnGluAlaValTyrTyrSerAspAsnAlaPro 195
    :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1184  CC.....GAACGGAGAAATTTGCTGTATGTTATGTCATCAATCAAAC 1227
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
196  IleSerAsn...ProAspGluSerPheLys.....204
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1228  CGTACCAATATTCCTTATGCGACCATGATTTATGGGATTTGGAAGGC 1277
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
205  .ArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetA 221
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1278  TCGTTCAATATCAACGCGACTTAGAAAACGACGCTAATCAATGATGTG 1327
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
221  rGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetPro 237
    :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1328  AGCTTGAGAGATTCAGGTCATGACATGCTGAAGCAAGAAATTTACA 1377
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
238  LysGlnValProAspAsp.....243
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1378  TCAAGTTATGGGGTTGATGTTACAAAACCTTATTAAACGCGATATCAC 1427
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
244  .....PheGlnLeuSerIlePheGluSerGluAspL 254
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1428  AGCAGGCGCTAGAAATGATGTTTCAAAATGACCAACGTCAGCAATGTG 1477
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
254  ySGIAspLys...TyrAsnLysGlyTyr.....262
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1478  TTGGAATTAATATCAAAATTAAGCATTTATCATCAAAAGTAACAGGAA 1527
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
263  .....GlnAsnLeuLeuSer.. 267
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1528  ACAGACCAATCTGTTAAGCCATTTGTTGTTCAATCCAAATTTGGCAAG 1577
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268  .....GlyGly.....269
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1578  TCGTGTGCTTCTGATATATGCTGCTTTTACTCAGTTGAGAGAAATGCT 1627
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
270  .....LeuValProThrLysProProThrProGly 279
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1628  ACTTCAAAACGAATTTGCCCTGTCTCTCTTAAGAGGTAGTGTCTGGG 1677
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
280  AspProPheMetProProAsnGlnProGlnThrThrSerValIleArg 296
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1678  AAAAGTGAATTT.....ACTAAGCCCTTATTTACAGTAGCAAAATCTA 1721
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
296  gLysTyrAlaIleGlyAspTyrSerLysLeu.....L 307
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1722  ACGAGTGGCTGACCTTGCTTTAAGAAATGTCAACTGACATGTGCCAT 1771
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
307  euGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGln 323
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1772  TGCCAGAGGCGGCTTTGAGCTGCTTCATCAATGCTAATAGT...CAG 1818
    :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
324  AlaArgValPheSerSerAspIleGlyGlu.....ArgIleGluLe 338
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355 er..... 355
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356 IleAlaGluProIleThrPhe.....LysValG1 365
1969 GCTGAGAAATGTGCTACTGTGGGAAGCCACATTCGTCTGTAAGTAGA 2018
365 uAlaGlyLysValThrIleIleAspGlyLysGln...IleGluAsn 381
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381 roAsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPhe 397
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2130 ACTGTGCAAAATGTCA..... 2148
431 euLysSerProAspSerGlnAspGlyLysThrMetThrProAsp 447
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448 PheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeuP 464
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619 gThrLysAspPheHisPheGluIleGlu.....LeuLysAsnA 632
2775 TACTGTGAAAGACTCAGCCCAAGTGTATACCTTATCAGGTTTATCAAGTG 2824
632 snLysGlnGluLeuLeuSerGlnThrValLysThrAspLys...ThrAsn 647
2825 AGCAAGGTCAAGTCGGTGATATGACAAATGAGAAGATAGTACCAT 2874
648 LeuGluPheLys.....AspGlyLys.....AlaThr 656
2875 ATTAATTCCTCAAAACGTGATATTGACGCAAGAGATTACGTGTCGAC 2924
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3166 GGTTCAGGTCAAGTTATGATATTGAAGAAAGCTT 3201
seq_name: /cgn1_7/plodata/1/lna/5B_COMB.seq:US-08-447-031A-8
seq_documentation_block:
; Sequence 8: Application US/08447031A
; Patent No. 5851794
; GENERAL INFORMATION:
; APPLICANT: GUS, Bengt
; APPLICANT: HOOK, Magnus
; APPLICANT: JONSSON, Hans
; APPLICANT: LINDBERG, Martin
; APPLICANT: PARTI, Joseph
; APPLICANT: SIGNAS, Christer
; APPLICANT: SWITALSKI, Lech
; TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,031A
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00707
FILING DATE: 22-OCT-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: SE 9003374-7
FILING DATE: 22-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 931..4485
US-08-447-031A-8

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  Quality: 149.00      Length: 774
  Ratio: 0.427        Gaps: 41
Percent Similarity: 45.090 Percent Identity: 19.251

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alignment block:

US-09-494-297-2 x US-08-447-031A-8 ..

Align seg 1/1 to: US-08-447-031A-8 from: 1 to: 4612

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99 GluGlySerArgSerTyrGlnValTyrCysPheAsnLeuys..... 112
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113 .....LysAlaPheProLeuGlySerAspSerValL 124
1785 TACCAATGACAGCAAAAGAGTTGTTAATTAATTCACAAGCT..... 1827
124 yslsTTPtYrLysLysHisAspGlyIleSerThrLysPheGluAspTyr 140
1828 .....TGTGATTCAGACCATGCT..... 1845
141 AlameSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAl 157
1846 .....AAGGAAGAAGTGAACGGCAATCATTTATCATCTG..... 1884
157 aValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly 173
1885 .....CACAATATTATGCTAATGCGCGATTCAGAGTA 1918
174 .....LeuGluProLeuAsnAlaIleArgValThrGlnGlu 185
1919 CTGTAAGAAGTGAATTAAGTTTAAACAGATTAAGATCAACAG... 1965
186 AlavalTrpTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSe 202

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1966 .....GCTCCTATAGCTAAT.....GTAA 1985
202 rPheLys...ArgGluSerGlnSerAsnLeuValSerThrSerGlnLeuS 218
1886 ATTTAAACTTTCTTAAAAAGATGCATCGTTGTAAGACATCA... 2031
218 erLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThr 234
2032 .....AAGAAATTCAGATTATTAACAGATGCAACGCTATTGCT 2070
235 LysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSe 251
2071 AATATTAAAGCGTTGCCTAGCGAGACTATTTTAAAGAAATAGAGGC 2120
251 rGlu.....AspLysGlyAspLysTyr..... 258
2121 GCCACAGACCGTATACATTCAGGATATTGATAAGAAATATCCGTTACTATGA 2170
259 .....AsnLysGlyTyrGlnAsnLeuLeuSerGlyLysLeu... 270
2171 AAGTACAGATTAATCAGGATATTTTACGACTATTGAAATGCAAAAGCG 2220
271 .....ValProThrLysProProThrProGlyAspPr 281
2221 ATAGAAAAACAAAAGATGTTTCTGCTCAAAAGTTGGCAAGCAGCTCA 2270
281 oProMetProProAsnGlnProGlnThrThrSerValLeuIleArgLysT 298
2271 AAAAGTGAACCA.....ACGATTATTATTCAAATGTGT 2302
298 yAlaIleGlyAspTyrSer..... 304
2303 ACAAAACAGATGACAAATCAAAATACAAACCCAGTACAAACAGAGATT 2352
305 LysLeuLeuGlnGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSe 321
2353 AAAAATTAGAGATGGAAGACACAAAAGTGATGCTGCTATCTT... 2397
321 rPheGlnAlaArgValPheSerSerAsnAsp...IleGlyGluArgIleG 337
2398 .....CCGAAATATGACAAAATGCAAGGCTATTTA 2428
337 luleSerAspGlyThrTyrThrLeuThrGluLeuAsn..... 349
2429 AA.....TATTAGTTAAAGAAATGCTCAAGGTGAA 2463
350 .....SerProAlaGlyTyrSerIleAlaGlu..... 358
2464 GATACAAACCCAGAGATATCTAAAAAAGAAATGTTTAGTGTTAC 2513
359 .....ProIle...ThrPheLysValGluAlaGlyLysValT 370
2514 TAATACTGMAAAACCAATCGAACACATCAATTAGTGTAAAGATAT 2563
370 yrrThrIleIleAspGlyLysGlnIleGluAsnProAsnLysGlnIleVal 386
2564 GGGACGACAAAGACAAATCAAGATGTAAGACACCAAAAA... 2604
387 GluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerValle 403
2605 .....GTCAGTGTCAATTATTTGGCTAACCGGAGCAAAAGTAAACGTT 2648
403 uThrThrGlnAsnTyrAlaLysPheTyrTyr.....AlaL 415
2649 AGAGCTGACATCTGAACAACTGCAAGTACGAATTTAAAGACTTACGA 2698
415 yAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeu 431
2699 AGTATGATGAAGA...AAGAAATAGAAATATATACATGACCGAAGATCAC 2745
432 LysSerProProAspSerGluAspGlyGlyLysThrMetThrProAspPh 448
2746 GTAAAGACTACACACAGACATCAACGCTACGACATTAACGAACAGTA 2795

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## alignment\_scores:

Quality: 148.00 Length: 843  
 Ratio: 0.393 Gaps: 43  
 Percent Similarity: 44.721 Percent Identity: 19.336

## alignment\_block:

US-09-494-297-2 x US-08-447-031A-1 ..

Align seg 1/1 to: US-08-447-031A-1 from: 1 to: 3827

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64  ProkopserserSerGIuTYrArgTYrP.....GIuTYrGI 76
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694  CCAGAGATGACGACACATGACCATGCTTTTAAATATATACAAATGAAA 743
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
76  uSerTYrValArgGIyHISProTYrTYrLys.....G 87
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
744  AAGTTAGTATCGAAGATATATCTATAAGATTCAGATTCAGGCGAC 793
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
87  InPheArgValAlaHISAspLeuArgValAsnLeuGIuGlySerArgSer 103
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
794  AGCAGTAGATTTAAGCACAATTAAACATTAATGTGACAGGTACACATAGC 843
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
104  Tyr.....GInValTYrCYsPheAsnLeuLysLysAlaPhePr 116
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
844  AATTATATAGTGACAAAGTCACATTAATGATTTGAAAAAGCCTTCC 893
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
116  OLeuGIySer.....AspSers 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
894  A...GGTCTAATAATACCTGTGATATACGAAGAACACAAATGATGTA 940
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
122  erValLysLysTYrTYrLysLysHISAspLylIeSerThrLysPheGIu 138
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
941  CAATTCACACAGGTATGCTATATATATGTTTTCATTAATTAATACACAA 990
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
139  AspTYrAlaMetSerProArgIleThrGIy..... 148
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
991  .....ACCAAAATTAAGAAATGAACAGCAAAAAAGCTTGT 1025
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
149  .....AspGIuLeuAsnG 153
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
1026  TAATTAATTCACAGCTGTGATATACAGACATGTAAGAAAGATGTAAGC 1075
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153  InLysLeuArgAlaValMetTYrAsnGIyHISProGInAsnAlaAsnGIy 169
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1076  GGA...TCATTAATCATACTGTGCACAAATATTAATGCTAATGCC 1119
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170  IleMetGIuGIy.....LeuGIuProLeuAsnAlaIleAr 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
1120  GGTATTTGAAGTACTGTAAGAAAGTGAATTAAGTTTAAACAGCATAA 1169
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
181  gValThrGIuGIuAlaValTYrTYrSerAspAsnAlaProIleSera 198
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
1170  AGATTAACAG.....GCTCCTATFACCTA 1192
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
198  snProAspGIuSerPheLys...ArgGIuSerGIuSerAsnLeuValSer 213
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1193  AT.....GTAAATTTAACTTTCTTAAAAAAAGATGATCAGTTGTAAG 1236
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
214  ThrSerGIuLeuSerLeuMetArgAlaAlaLeuLysGIuLeuIleAspPr 230
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1237  GACATATCA.....AAGAAATTAAGATTAATTAACAGATGC 1271
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230  oAsnLeuAlaThrLysMetProLysGIuValProAspAspPheGInLeuS 247
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
1272  AAACGGTATTGCTAATATTAAGGTTGCTAGAGACACTATATTTTAA 1321
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
247  erIlePheGIuSerGIu.....AspLysGIyAspLysTYr 258
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
1322  AAGAAATTAAGAGCCGACAGACGCTATACATTTGTAAGATTAAGAAATAT 1371
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259  .....AsnLysGIyTYrGIuAsnLeuLeuSe 267
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267  rGIyGIyLeu.....ValProThrLysProProT 277
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1422  AAATGCAAAAGCGATAGAAAAACAAAAGATGTTCTGCTCAAAAGGTTT 1471
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277  hrProGIyAspProPheMetProProAsnGInProGInThrThrSerVal 293
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1472  GCGAAGGCACTCAAAAAGTGAAACCA.....ACGAT 1503
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294  LeuIleArgLysTYrAlaIleGIyAspTYrSer..... 304
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1504  TATTTCAAGTTGTACAAACAAAGATGACATCAAAATACACACACAGTAGA 1553
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305  .....LysLeuLeuGIuGIyAlaThrLeuGIuLeuThrGIyAla 317
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1554  CAAGACAGATTTAAAAATTAAGAAATGACAGCAAAAGTGCATAGT 1603
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317  sPAsnValAsnSerPheGInAlaArgValPheSerSerAsnAsp...Ile 332
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333  GIyGIuArgIleGIuLeuSerAspGIyThrTYrThrLeuThrGIuLeuAs 349
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349  n.....SerProAlaGIyTYrSerIleAlaGIu... 358
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1665  TGCTCAAGTGACATACAAACACAGAGATATATCAAAAAGAAATG 1714
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359  .....ProIle...ThrPheLysValGIu 365
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1715  GTTTAGTGTTACTAATACGAAAAACCAATCGAAACATCAATATAGT 1764
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366  AlAGlyLysValTYrThrIleIleAspGIyLysGInIleGIuAsnProAs 382
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1765  GGTAAAAAAGTATGAGCAGCAAAAGACATCAAGATGTAAGAACCAAGA 1814
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382  nLysGIuIleValGIuProTYrSerValGIuAlaTYrAsnAspPheGIuG 399
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1815  AAAA.....GTCAGTGTAATTTATGCTAACGGGAGA 1849
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399  LuPheSerValLeuThrThrGIuAsnTYrAlaLysPheTYrTYr..... 413
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414  .....AlaLysAsnLysAsnGIySerSerGIuValValTYrCYsPh 427
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1900  AAAGACTTACCGAAGTATGATGAAGGA...AAGAAATATCAATATTAAGT 1946
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427  eAsnAlaAspLeuLysSerProProAspSerGIuAspGIyLysTYrThm 444
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1947  GACCGAAGATCAGCTAATAAGACTACACACAGACATCAACGGTACGACAA 1996
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444  eThrProAspPheThrThrGIyGIuValLysTYrThrHISIleAlaGIy 460
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1997  TAAGCAACAAGTATACACAGAGACATCGCCACAGTAACAAAAAAT 2046
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461  ArgAspLeuPheLysTYrThrValLysProArgAspThrAspProAspTh 477
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628 .....GluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrV 641  
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697 AsnAlaThrValSerLys.....ThrGlyIleThrse 707  
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707 raspgLutThrLeuAlaPheGluAsnAsnLysGluProValValProThrG 724  
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2889 TGAATAAGTATGGGACGACCAAGCAATCAAGATGTAAGAGACCGAGAAA 2938  
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2939 AACCTGATGTCGAATTTATTTGGCTAACGCA 2967  
seq\_name: /cgn1\_7/ptodata/1/lna/5A.COMB.seq:US-08-703-947-1  
seq\_documentation\_block:  
; Sequence 1, Application US/08703947

Patent No. 5788962  
GENERAL INFORMATION:  
APPLICANT: Wise, Kim S.  
APPLICANT: McIntosh, Mark A.  
TITLE OF INVENTION: DNA Sequences Coding for Mycoplasma  
TITLE OF INVENTION: Hypneumonae Surface Antigens,  
TITLE OF INVENTION: Corresponding Proteins and Use in  
TITLE OF INVENTION: Vaccines and Diagnostic Procedures  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Grace J. Fishel  
STREET: 929 Fee Fee Road, Suite 100  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63043  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage  
COMPUTER: Hewlett-Packard Vectra  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/703,947  
FILING DATE: 28-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/373,957  
FILING DATE: January 17, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fishel, Grace J.  
REGISTRATION NUMBER: 25864  
REFERENCE/DOCKET NUMBER: UVA 8141  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 878-0440  
TELEFAX: (314) 275-7693  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2672 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
DESCRIPTION: region of 5.8 kb HindIII fragment from  
DESCRIPTION: genomic library  
HYPOTHETICAL: no  
ANTI-SENSE: no  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: Mycoplasma hypneumonae  
STRAIN: J  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: unicellular bacterium  
CELL LINE:  
ORGANELLER:  
IMMEDIATE SOURCE:  
LIBRARY: Genomic in Charon 4A, GEN12  
CLONE: MhpJ25, MhpJ35, pZJ25, pZJ25.1, pZJ25.14,  
CLONE: pZJ35.1, pZJ35.12, pZJ35.13, pZJ35.14  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: single chromosome  
MAP POSITION: unknown  
UNITS: unknown  
FEATURE:  
NAME/KEY: sequence encodes entire 627 amino acids of  
NAME/KEY: the structural gene for the surface lipoprotein  
NAME/KEY: p65 and includes 312 bp upstream and 479  
NAME/KEY: bp downstream of coding sequence  
LOCATION: coding sequence for p65 spans 1881 bp of  
LOCATION: described sequence (begins at nt 313 and



LOCATION: includes all sequence through nt 2193  
IDENTIFICATION METHOD: by similarity to pattern of open reading  
IDENTIFICATION METHOD: frame: By experiment identifying protein products of  
IDENTIFICATION METHOD: sequence with immune serum to p65  
OTHER INFORMATION: Immunogenic surface lipoprotein of no known  
OTHER INFORMATION: function: C-terminus exposed on external  
OTHER INFORMATION: surface of cell  
PUBLICATION INFORMATION:  
AUTHORS: Mary F. Kim, Manijeh B. Heidari, Susan J.  
AUTHORS: Stull, Mark A. McIntosh, and Kim S. Wise  
TITLE: Identification and Mapping of an  
TITLE: Immunogenic Region of Mycoplasma  
TITLE: hyopneumoniae p65 Surface Lipoprotein  
TITLE: Expressed in Escherichia coli from a Cloned  
TITLE: Genomic Fragment  
JOURNAL: Infection and Immunity  
VOLUME: 58  
ISSUE: 8  
PAGES: 2637-2643  
DATE: August 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: From 1 to 2672

1440 ..... 1440  
441 ylysthrmetThProaspheThrThrglygluValylsTyThrhist 458  
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1441 ..... GAC 1443  
475 ProAspThrPheLeuLysHisIleLysLysValIleGluLysGlyTyThr 491  
1444 CTAGAGTCTTTGCAAAATCAAAATTAAGAAATTCCTGAAAAA...TTAAA 1490  
491 ggIuLysGlyGlnAlaIleGluTySerGlyLeuThrGluThrGlnLeu 508  
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1610 TACCAATCTTCGAAATTTGATTTAGAGATTAATACCTGTTAAAT 1659  
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666 rIeugInGlyLeuProGluGlyTySerTy..... 676  
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seq\_documentation\_block:  
; Sequence 9, Application US/08480604A  
; Patent No. 5736139  
; GENERAL INFORMATION:  
; APPLICANT: KINK, JOHN A.  
; APPLICANT: THALLEY, BRUCE S.  
; APPLICANT: PADHYE, NISHA V.  
; APPLICANT: FIRCA, JOSEPH R.  
; APPLICANT: STAFFORD, DOUGLAS C.  
; TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,604A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/422,711  
; FILING DATE: 14-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/405,496  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/329,154  
; FILING DATE: 25-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/161,907  
; FILING DATE: 02-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/985,321  
; FILING DATE: 04-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/429,791  
; FILING DATE: 31-OCT-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: INGOLIA, DIANE E.  
; REGISTRATION NUMBER: 40,027  
; REFERENCE/DOCKET NUMBER: OPD-01763  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7101 base pairs  
; TYPE: nucleic acid

[illegible]

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seq\_name: /cgn1\_7/pdata/1/lna/5B\_COMB.seq:US-08-405-496A-9

seq\_documentation\_block:  
 ; Sequence 9, Application US/08405496A  
 ; Patent No. 5919665  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILLIAMS, JAMES A.  
 ; TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM

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; TITLE OF INVENTION: NEUROTOXIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,496A
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/329,154
; FILING DATE: 25-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,907
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,321
; FILING DATE: 04-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/429,791
; FILING DATE: 31-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: INGOLTA, DIANE E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: OPND-01308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7101 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..7098
; US-08-405-496A-9
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seq_documentation_block:
; Sequence 7, Application us/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du

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APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-ping
APPLICANT: Kiehn, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSER: Slim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2682 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-074-658-7

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364 LgAlaLagLysValtYrThrLLeLLeAspGlyLysGlnLLeGluAsnP 381
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1461 GGAATATGAACGATTTGGTGAATATTTAGCCGTAAAGGTTAAATATATC 1510
381 ro...AsnLysGluLLeValGluProTtYrSerValGluAlaTtYr..... 394
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1511 ACATATATAGAAGATGAATATATCCAGTGATGATGTTATGTATGATAT 1560
395 .....AsnAspPheGluGluPheSerValLeuThrTh 405
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1561 ACTTGGGCAAGCCAGAGAGAGTTCACCAAAAAGTACGACGACGAC 1610

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405 rgl.....AsnTyrAlaLysPheTyrTyrAlaL 415
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1611 CCAAGTCGTGCCACCTTATTTTGGCAGACATGATAATTTTATTTT... 1656
415 ysaAnLysAnGlySerSerGlnValValTyrCysPheAsnAlaSplu 431
    |||||
1657 .....AATGGCACTATTATGACCTATACGACGAGTGTGTGATAAA 1698
432 LysSerProAspSerSerGluAspGlyLysTyrMetThrProAspPh 448
    |||||
1699 TTAGCCCTGCGGATGCTGTCAAGCCAAACCAATCCATTAAGAAAAATA 1748
448 eThrThrGlyLysVal..... 453
    : : : : :
1749 CCTAATGCCACTAAATAAGAACCAAGTTACGCCATCGTCTAC 1798
454 .....LysTyr 455
1799 AAGAAGCCAAAGATATATAGCCTTATACGCCATTCGTGCCAAAAGCTAT 1848
456 ThrHisIleAla...GlyArgAspLeuPhe..... 464
    |||||
1849 CAGACATCAGTTTGGCGAGACGCTGATATAAGATGCCCAACAAACCC 1898
465 .....LysTyrThrValLysProArgAspThrAspProAspThrPheL 479
    |||||
1899 AACACGCAAGTTATTTTGTCAAGCGGTAGGCGAGATACCGACACACT 1948
479 eulYsHisIleLysLysValIle..... 486
    |||
1949 TGCCCCCAGCGAGTAAATTCACCTACAAAGCTTTGGCGAGCTACTCG 1998
487 .....GluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyr 499
    |||||
1999 ACCCAAAAAAGACAAAGTTATAGCATATGACAAACATCAACAGGA 2048
499 rSerGly.....LeuThrGluThrGlnLeuArgAlaIalal 511
    |||||
2049 AAAAGGTCATCCAGGTATATCTTACCGAAAC..... 2082
511 hrGlnLeuAlaIleTyrTyrPheThr.....AspSer 521
    |||||
2083 .....TTCACCCCAAGATGATGACGATGATTG 2112
522 AlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMe 538
    |||
2113 ACCGCATCTGATGATTCACAGATGATATACATGCGCATGATGATT 2162
538 tAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnA 555
    |||
2163 G.....ATTCATCTGATGATTACACAG 2185
555 spSerAsnProGlnLeuThrAspLeuAspPheIleProAsnAsn 571
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2186 ATGATGACGCGATGAGATGACATTCAGATGATTG.....GGTGAT 2229
572 AsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuVa 588
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2230 GGTCAGATGATGACGCGCGCAAGGTATATCATGCAAGTAT..... 2274
588 lAspIleIleArgMetGluAspLysGlyGlnValIleProVal..... 602
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2275 .....ATTGCGCCCTGAATTTGAACAAATACTGCCCTTAATGAGC 2317
603 ..ThrHisAsnLeuThrLeu..... 608
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2318 CTACTCATGAATAAACCTTTCCTAGATGCTAAATAAAGCTAAGTTT 2367
609 .....ArgLysThrValThrGlyLeuAlaGlyAspArgTh 620
2368 GAAGTGATTTTAAACACACAGCCTAAGCTTAATTAACGATGAGAG 2417

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620 rLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnLeuL 637
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637 euSerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAspGly 653
    |||||
2462 CAGATTTACGCCCAAGCCGATGCGCAAACTATTCGTGAAGAAGTGCGT 2511
654 LysAlaThrIleAsnLeuLysHisGlyLysLeuThrLeuGlnGlyLe 670
    |||
2512 .....AACACCAAGGTGCG..... 2526
670 uProGlnLysTyrSerTyrLeuValLysGluThrAspSerGlnGlyTyrL 687
    |||||
2527 .....GGTTCTTATACACATCAACAGATTTGATGTTAAGGGCAAT 2569
687 yValLysValAsnSerGlnLysValAla..... 696
2570 TTTTGGCCAAATGGCGAAGAGTTGGCAGCAGATTACATCATGACAA 2619
697 .....AsnAlaThrValSerLysThrGly 704
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2620 GCGCATGCGCATCAATGACACCGCGCAAAACAGCG 2655
seq_name: /cgnl_7/ptodata/1/lna/5b_COMB.seq:us-08-867-941-6
seq_documentation_block:
; Sequence 6, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, QuiJun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; City: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-867-941-6
alignment_scores:
Quality: 138.00 Length: 812
Ratio: 0.408 Gaps: 39
Percent Similarity: 41.626 Percent Identity: 19.704

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## alignment block:

US-09-494-297-2 x US-08-867-941-6 ..

Align seg 1/1 to: US-08-867-941-6 from: 1 to: 7641

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84  TTTTTLTGLSGLNPhEaRgVAlAlAHISAsPLeuARgVAlAsnLeuGlu 100
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632  TATTTAACAATTCCTGATGTGTGATTTGCACTAGACAGTGAACG 681
    |||:::|||||::: |||:::|||||::: |||
100  ySerARgSerTYrGLNValTYrCySPheAsnLeuLYSLysAlaPheProL 117
    |||:::|||||::: |||:::|||||::: |||
682  CCATTCGT...TTTGACCCCAAAAGATTAACCATTAAGTGTAGCTT 728
    |||:::|||||::: |||:::|||||::: |||
117  euGLY.....SerAsPserSerValLYSLysTYrTYrLYSLysSHISAsP 131
    |||:::|||||::: |||:::|||||::: |||
729  ATGGTAACTTAACAACACCATCCACACACACACTCATCAATCATCAG 778
    |||:::|||||::: |||:::|||||::: |||
132  GLYLleSerThrLYSPheGLUAsPTYrAlaMetSerPro..... 144
    |||:::|||||::: |||:::|||||::: |||
779  CAAGCTGATTAATAAGAAATAACAGCCGTGTGACCCCTTATGAAATAT 828
    |||:::|||||::: |||:::|||||::: |||
145  .....ArgTLleThrGLYAsPGLULeuAsnGLNlys... 154
    |||:::|||||::: |||:::|||||::: |||
829  CCCTTTGGGTATCTTGAACTACAGAGACAGCTGACCCCAAAATG 878
    |||:::|||||::: |||:::|||||::: |||
155  .....LeuARgAlaVal 158
    |||:::|||||::: |||:::|||||::: |||
879  CCGATTAATCAAAATGACCAAGACCGCATCCCAAAACCATGCCATTG 928
    |||:::|||||::: |||:::|||||::: |||
159  MetTYrAsnGLNLYSProGLNAsnAlaAsnGLYlLeMetGLNGLYeuGL 175
    |||:::|||||::: |||:::|||||::: |||
929  TTTTATCATGA.....GAATAAGCCAGACAGCAGCTGCCAGCGCTGG 972
    |||:::|||||::: |||:::|||||::: |||
175  uProlLeuAsn..... 178
    |||:::|||||::: |||:::|||||::: |||
973  TAAATTTAACTACACAGCACTGGCTGTACTTAAGTATGCAAAAAAC 1022
    |||:::|||||::: |||:::|||||::: |||
179  ....AlaILeARgValThrGLNGLUAlaValTYrTYrSerAsPasn 193
    |||:::|||||::: |||:::|||||::: |||
1023  GCCCTGCCCTTTCAGCATCAGATGAGGAGTGGGGCTCTATCAATGCC 1072
    |||:::|||||::: |||:::|||||::: |||
194  AlaProlLeuSerAsnProAsPGLUserPheLYsARgLUserGLUserAs 210
    |||:::|||||::: |||:::|||||::: |||
1073  AGTGGCAAAAGCCAAC.....GAGGGCGA 1095
    |||:::|||||::: |||:::|||||::: |||
227  euILeAsPProAsnLeuAlaThrLYSMetProLYsGLNValProAsPasp 243
    |||:::|||||::: |||:::|||||::: |||
1145  .....ACGCCCTGCCACTTATCAGGTGGATTTTGAC 1174
    |||:::|||||::: |||:::|||||::: |||
244  Phe.....GLNLeuSerILePheGLUserGLUAsPlySGl 255
    |||:::|||||::: |||:::|||||::: |||
1175  ACAAACTCATTAACAGCAAGCTGTCTATTATATGACAATCCCAATCAG.. 1222
    |||:::|||||::: |||:::|||||::: |||
255  yASpLYsTYrAsnLYsGLY..... 261
    |||:::|||||::: |||:::|||||::: |||
1223  ....CAAAATAATTAAGCGCAATATCTCAAAAGCCAAATTTGACACTACA 1268
    |||:::|||||::: |||:::|||||::: |||
262  .....TyrgLn..... 263
    |||:::|||||::: |||:::|||||::: |||
1269  AAAAAGTCATGAACCGATGTGTATCAATTTGATGCCAAAATACAAGCT 1318
    |||:::|||||::: |||:::|||||::: |||
264  AsnLeuLeuSerGLY.....GLYLeuValProThrLYsProProTh 277
    |||:::|||||::: |||:::|||||::: |||
1319  AACCGCTTTGTGCGTAGCGCAAAATCTTGGTTATATGAGAAACAACAAC 1368
    |||:::|||||::: |||:::|||||::: |||
277  rProGLY.....AsPProProMetProProAsnGLNp 288
    |||:::|||||::: |||:::|||||::: |||
1369  CGGACCTTTTATCAAAAGAGCTGTCTCAAAAAAGCCAAACCCCAATTAAC 1418
    |||:::|||||::: |||:::|||||::: |||

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```

288  roGLNThrThrSerValLeuILeARgLYsTYrAlaILeGLYAsPTYrSer 304
    |||:::|||||::: |||:::|||||::: |||
1419  CAAACCTTAAT.....TCA 1432
    |||:::|||||::: |||:::|||||::: |||
305  LysLeuLeuGLNGLYAlaThrLeuGLNLeuThrGLYAsPasnValAsnSe 321
    |||:::|||||::: |||:::|||||::: |||
1433  GACACCTGTGAAGCGGATTTATGTGTGAGTCGGGCAATGAGCTG..... 1477
    |||:::|||||::: |||:::|||||::: |||
321  rPheGLNAlaARgValPheSerSerAsnAsPle..... 332
    |||:::|||||::: |||:::|||||::: |||
1478  .....GGCGGTAAATTTTATCAATGACAAACGATCTATGTGTGT 1520
    |||:::|||||::: |||:::|||||::: |||
333  ....GLYAlaRgILeGLULeuSerAsPGLYsTYrThrThrLeuThrGLU 347
    |||:::|||||::: |||:::|||||::: |||
1521  TTGGTGCAAAACGAGCAAAACGACTAAACCTGTCCGCAAAAAGCGGTG 1570
    |||:::|||||::: |||:::|||||::: |||
348  LeuAsnSerProAlaGLYTYrSerILeAlaGLUProILeThrPheLYsVal 364
    |||:::|||||::: |||:::|||||::: |||
1571  TATTTTAgT...GCAGGCTTTGAA.....AAACCAAGCACCGATTGTTGT 1611
    |||:::|||||::: |||:::|||||::: |||
364  lGLUAlaGLYLYsValTYrThrILeILeAsPGLYsGLNlLeGLUAsnP 381
    |||:::|||||::: |||:::|||||::: |||
1612  GGATTAATGAACGATTGTGTGAATTTATGACGTTAAAGGTTAAATATTC 1661
    |||:::|||||::: |||:::|||||::: |||
381  ro...AsnLYsGLUleValAlaGLUProTYrSerValAlaValTYr..... 394
    |||:::|||||::: |||:::|||||::: |||
1662  ACATTTATGAAGATGAATAATTATCCAGTATGATAGTATTTATGATAT 1711
    |||:::|||||::: |||:::|||||::: |||
395  .....AsnAsPheGLUGLUpheserValLeuThrTh 405
    |||:::|||||::: |||:::|||||::: |||
1712  ACTTTGGGGCAAGCAGAGAGAGAGCTTACCAAAAAGTCAGCAGCAGCAC 1761
    |||:::|||||::: |||:::|||||::: |||
1762  CCAAGTCGTCCAGCTTATTTGGGCAACATGATTAATTTATTTT... 1807
    |||:::|||||::: |||:::|||||::: |||
415  ySAAsnLYsAsnGLYserSerGLNValValTYrCySPheAsnAlaAsPleu 431
    |||:::|||||::: |||:::|||||::: |||
1808  ....AATGGCACTATTATGACCTATACAGCCAGCTGTGTGATATAA 1849
    |||:::|||||::: |||:::|||||::: |||
432  LysSerProProAsPserGLUAsPGLYGLYsThrMetThrProAsPph 448
    |||:::|||||::: |||:::|||||::: |||
1850  TTAGCCCTCGCTCCGATGCTGTCAAAAGCCAAACCATTAAGAAAAATA 1899
    |||:::|||||::: |||:::|||||::: |||
448  eThrThrGLYLUVal..... 453
    |||:::|||||::: |||:::|||||::: |||
1900  CCTTAATGCCACACTAATAATAAGACAAACAAGTTACCGCATGTGTGTAC 1949
    |||:::|||||::: |||:::|||||::: |||
454  .....LysTYr 455
    |||:::|||||::: |||:::|||||::: |||
1950  AAGAAGCCAAAGATATAAGCTTATACCCCATTCGTGCCAAAAGCTAT 1999
    |||:::|||||::: |||:::|||||::: |||
456  ThrHisILeAla...GLYARgAsPLeuPhe..... 464
    |||:::|||||::: |||:::|||||::: |||
2000  CAGCAATCATGAGTTTGGCAGACGCTGTATTAACGATGCCAAACCAACCC 2049
    |||:::|||||::: |||:::|||||::: |||
465  ....LysTYrThrValLYsProARgAsPThrAsPProAsPThrPheL 479
    |||:::|||||::: |||:::|||||::: |||
2050  AACACGCAAGTTATTTTGTCAAGCGGTAGGCGAGATACACAGCACACTT 2099
    |||:::|||||::: |||:::|||||::: |||
479  euLYsHISILeLYsValLe..... 486
    |||:::|||||::: |||:::|||||::: |||
2100  TGCCCCAGGAGGTAATTCATTAACAAGGTCTTTGGCAGGCTACCTG 2149
    |||:::|||||::: |||:::|||||::: |||
487  .....GLYLYsGLYTYrARgLUlySGlYAlaILeGLYTY 499
    |||:::|||||::: |||:::|||||::: |||
2150  ACCCAAAAAAAGGACAAAGGTTATAGGATTAATGCAAAACCATCAAGGA 2199
    |||:::|||||::: |||:::|||||::: |||
499  rSerGLY.....LeuThrGLUThrGLNLeuARgAlaVal 511
    |||:::|||||::: |||:::|||||::: |||
2200  AAAAGTCAATCAGGTTATCTGTTAACGAAAAAC..... 2233
    |||:::|||||::: |||:::|||||::: |||

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511 hrcglnleualalelyrtyrpheth.....aspser 521
2234 .....ttcacccccaagatgatgcagtatttg 2263
522 alaglualeasplysasplyseulyasaptyrhiasglyphegluaspe 538
::: ||| :::: | ||||| |||
2264 accgcattgatgatgtacacaagatgataatpacscatggcgatgatgtt 2313
538 tasinaspserthrleualaialalalslileuevalglutyralsglna 555
: ||| :::: | |||
2314 g.....attgcantctgatgattcacaag 2336
555 spserasnproproginleuthraspleuaspherheileprodanasn 571
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|||||::: |||||
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2663 .....aacaccacaagtgcc..... 2677
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||::: ||| ::||| |||
2678 .....ggttcttatnacacatcaaaatattgttataggggcaat 2720
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::: ||||| ||||| |||
2721 wttttggcacaatgcccgaaggttgagagacgttacatcatgacaaa 2770
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||| ||||| ||||| |||
2771 gccgatggcatcaatgacacccgccgaaaaagcagg 2806

seq_name: /cgn1_7/ptodate/1/ina/6B_COMB.seq:US-09-074-658-6
seq_documentation_block:
? Sequence 6, Application US/09074658
? Patent No. 6184371
? GENERAL INFORMATION:
? APPLICANT: Loosmore, Sheena M
? APPLICANT: Run-Pan Du
? APPLICANT: Quliun Wang
? APPLICANT: Yang, Yan-Ping
? APPLICANT: Klein, Michel H
? TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
? NUMBER OF SEQUENCES: 78
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Sim & McBurney
? STREET: 6th Floor, 330 University Avenue
? CITY: Toronto
```

STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,658  
FILING DATE: 08-MAY-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-795  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7641 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

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alignment_scores: 100 00
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Quality:	138.00	Length:	818
Ratio:	0.408	Gaps:	39
Percent Similarity:	41.626	Percent Identity:	19.704

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alignment_block:
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Align seg 1/1 to: US-09-074-658-6 from: 1 to: 7641

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      632  TATTTTAACAATTCCTCGCATGTCTGATTTGGACCTTAGCACTGAACG 681
      100  ySerArgSerTyrGlnValTyrCySPheAsnLeuLysLysAlaPheProL 117
      |||:::|||||:::|||||:::|||||:::
      682  CCATCGT...TTTGACCCCCAAAAGATTAACACCATTAAGTATGATG 728
      117  euGLy.....SerAspSerValLysLysTyrTyrLysHisasp 131
      |||:::|||||:::|||||:::|||||:::
      729  ATGGTAACTTAAACAACCAACATCCAAACAACAACACTCATCAATCATCATG 778
      132  GlyLeSerThrLysPheGlnAspTyrAlaMetSerP..... 144
      |||:::|||||:::|||||:::|||||:::
      779  CAAGCTGATATATAGAAATAATTAACAACGCTGTGTGACCTTATGAAATAT 828
      145  .....ArgLeIthrGlyAspGluLeuAsnGlnLys... 154
      829  CGGTTTGGGTACTTGGAACTACAGAGAACGAGCTGACCCAAAAAATG 878
      155  .....LeuArGAlaVal 158
      |||:::|||||:::|||||:::
      879  CCGATATATCAAAATGAGCAAGACCGCATTCGCCAAACCATGCTATTGTG 928
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      |||:::|||||:::|||||:::|||||:::
      929  TTTTAACTACATGA...GA AAAACGCCAGAGCCAGCGAGTGCCTCAACGCGTGG 972
      175  uProLeuAsn..... 178
      |||:::|||||:::|||||:::
      973  TAAATTTAACTACACAGCAACGCGCTGTACCTTAAGATGTCAAAAAAAC 1022
      179  ....AlaIleArGvAlThrGlnGluAlaValTyrTyrSerAspAsn 193
      |||:::|||||:::|||||:::|||||:::
      1023  GCCCTGGCCCTTTCAGCATGAGTACGAGTGGGAGTGGCTATCTCAAAAGCC 1072Z

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194 AlaProIleSerAsnProAspGluSerPheLysArgGluSerGluSerAsp 210  
 1073 AGTGGCAAGCCAC.....GAGGGCGA 1095  
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 1096 TGTGCTGAGTGGCCGCCCATTTATCTAAACGGCTTCAATATATAGCAC. 1144  
 227 euIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAsp 243  
 1145 .....ACGCTGCCACTATTCAGGTGGATTTTGAC.1174  
 244 Phe.....GlnLeuSerIlePheGluSerGluAspLysGln 255  
 1175 ACAACATCATTAACAGCAGCTGTCTTATTTATGACATCCCAATCAG. 1222  
 255 yAspLysTyrAsnLysGly..... 261  
 1223 .....CAAAATATATAAGCGCAATATCTCAAAAGCCAAATTGACACTACA 1268  
 262 .....TyrGln..... 263  
 1269 AAAAAGTCAATGAACCCGATGTATCAAAATTGATGCCAAATCAACGGT 1318  
 264 AsnLeuLeuSerGly.....GlyLeuValProThrLysProProTh 277  
 1319 AACCGCTTTGTGCTAGCGCCAAATCTTTGGTTATGAGAAAACACAAC 1368  
 277 rProGly.....AspProProMetProProAsnGlnP 288  
 1369 CGCAGCTTTATCAAGAGCTGTCTCCAAAAAGCCCAACCCCAATAC 1418  
 288 roGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSer 304  
 1419 CAACCCCTAAT.....TCA 1432  
 305 LysLeuGluGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsn 321  
 1433 GACAGCTAGAACGGCGATTTATGCTGAGTCGGCGCATGAGCTG..... 1477  
 321 rPheGlnAlaArgValPheSerSerAsnAspIle..... 332  
 1478 .....GCCGGTAATTTTATTCATCAACAGCATCTTATGTGCT 1520  
 333 .....GlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu 347  
 1521 TTGGTGGCAACGACGACAAAACGACTAACCTGTGCCCAAAAAACGGTG 1570  
 348 LeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysVal 364  
 1571 TATTTTGT...GCAGCTTTGAA.....AAACCGACACGACTTTGT 1611  
 364 lGluAlaGlyLysValTyrThrIleIleAspGlyLysGlnIleGluAsn 381  
 1612 GCATTAATGAACGATGTGTAATTTATGACCCGTAAGGTTAAATATC 1661  
 381 ro...AsnLysGluIleValGluProTyrSerValGluAlaTyr..... 394  
 1662 ACATTAATGAAGATGAATATTCACGATGATGATTAATGAGTAT 1711  
 395 .....AsnAspPheGluGluPheSerValLeuThrTh 405  
 1712 ACTTTGGGCAAGCCAGAGAACGACTTACCAAAAAAGTCACAGCAGACAC 1761  
 405 rGln.....AsnTyrAlaLysPheTyrTyrAlaL 415  
 1762 CCAAGTGTGTCACAGCTATTTTGGGCAACATGATTAATTTATTTT... 1807  
 415 yAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeu 431  
 1808 .....AATGGCACTATTAATGACCTATCAGCCAGTGTGTTGATMAA 1849

432 LysSerProAspSerSerGluAspGlyLysThrMetThrProAspH 448  
 1850 TTAGCCCTGCCATGCTGTCAAAAGCCAAACCAATCCATTAAAGAAAAATA 1899  
 448 eThrThrGlyGluVal..... 453  
 1900 CCTTAATGACACACTAATAATAGACAAACCAAGTATCCCGCATGTGTAC 1949  
 454 .....LysTyr 455  
 1950 AAGAGCCAAAGATATATACCTTATACCCCATTCGTGCCAAAAAGCTAT 1999  
 456 ThrIleIleAla...GlyArgAspLeuPhe..... 464  
 2000 CAGACATCATGTTTGGCAGACGCTGTATACGATGCCAACCAACACCC 2049  
 465 .....LysTyrThrValLysProArgAspThrAspProAspThrPheL 479  
 2050 AACACGAGTTATTTGTGCAGCGGTAGGCGAGATACGACACCACTT 2099  
 479 euLysHisIleLysLysValIle..... 486  
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 487 .....GluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyr 499  
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 499 rSerGly.....LeuThrGluThrGlnLeuAlaAlaLar 511  
 2200 AAAAGTCATCAGCTTATCTGTAAACCGAAAC..... 2233  
 511 hrGlnLeuAlaIleTyrTyrPheThr.....AspSer 521  
 2234 .....TTCACCCCAAGATGATGACGATGATTG 2263  
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 2264 ACCGATCTGATGATTCACAAAGATGATATACATGCGCATGATGTTT 2313  
 538 LAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGln 555  
 2314 G.....ATTGCATCTGATGATTCACAAAG 2336  
 555 sPseAsnProProGlnLeuThrAspLeuAspPhePheIleProAsn 571  
 2337 ATGATGACGACATGAGATGACGATTCACATGATTG.....GGTAT 2380  
 572 AsnLysTyrGlnSerLeuIleGlyThrGlnThrHisProGluAspLeu 588  
 2381 GGTGCATGATGATGACCGCGCAAGCAAGTATCATCATCAGTAT..... 2425  
 588 lAspIleIleArgMetGluAspLysLysGluValIleProVal..... 602  
 2426 .....ATTGCCCTGAATTTGAAACAAATACTTCCCATTAATAGAC 2468  
 603 ...ThrHisAsnLeuThrLeu..... 608  
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 609 .....ArgLysThrValThrGlyLeuAlaGlyAspArgTh 620  
 2519 GAAGTGATTTTAACACCAACAGCTTAACGTAAATTAACGTAGAG 2568  
 620 rLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnLeuL 637  
 2569 AGGTGATATCGTCTTCATATC.....AAAAATGCGCAAAATGATGCGCA 2612  
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 2613 CAGGATTTACCGCAAAAGCGATGTGCCAAACTATCTGAAAGAGTGGT 2662  
 654 LysAlaThrIleAsnLeuLysHisGlyGluSerLeuThrLeuGlnGlyLe 670

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2663 .....AACACCAAGTGC..... 2677
      |||  :::  |||
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2678 .....GTTTCTTATACACATCCAAAGATATTGATCTTAAGGGCAAT 2720
      :::|||:::  |||:::  |||
687 ysValLysValAsnSerGlnGluValAla..... 696
      :::|||:::  |||:::  |||
2721 TTTTGGCACAATGGCGAGAGTTGGCAGACAGTTACATCATGCACAA 2770
      |||  |||  |||:::  |||:::  |||
697 .....AsnAlaThrValSerLysThrGly 704
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2771 GCGCATGGCATCATGACACCGCCGAAAAAGCAGG 2806
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